SEQUENCE LISTING

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<130> 2293.082PC03/PAC/KBK

<140> PCT/US2012/046746
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<150> US 61/570,629
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<151> 2011-07-15

<160> 76

<170> PatentIn version 3.5

<210> 1
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<212> PRT
<213> Homo sapiens

<400> 1

Met Arg Leu Gly Leu Cys Val Val Ala Leu Val Leu Ser Trp Thr His
1 5 10 15

Leu Thr Ile Ser Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile
20 25 30

Ser Ala Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser
35 40 45

Glu Val Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu
50 55 60

Glu Arg Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro
65 70 75 80

Pro Gly Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys
85 90 95

Cys Lys Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr
100 105 110

Lys Cys Lys Glu Gly Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala
115 120 125

```
Cys Pro Glu Gly Ser Ser Ala Ala Asn Gly Thr Met Glu Cys Ser Ser
    130                 135                 140

Pro Ala Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser
145                 150                 155                 160

Lys Lys Gln Gln Leu Cys Gly Phe Arg Arg Gly Ser Glu Glu Arg Thr
                165                 170                 175

Arg Arg Val Leu His Ala Pro Val Gly Asp His Ala Ala Cys Ser Asp
            180                 185                 190

Thr Lys Glu Thr Arg Arg Cys Thr Val Arg Arg Val Pro Cys Pro Glu
        195                 200                 205

Gly Gln Lys Arg Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn Ala Asn
    210                 215                 220

Arg Asn Leu Ala Arg Lys Glu Ser Lys Glu Ala Gly Ala Gly Ser Arg
225                 230                 235                 240

Arg Arg Lys Gly Gln Gln Gln Gln Gln Gln Gly Thr Val Gly Pro
                245                 250                 255

Leu Thr Ser Ala Gly Pro Ala
            260
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<210> 2
<211> 243
<212> PRT
<213> Homo sapiens

<400> 2

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Met Gln Phe Arg Leu Phe Ser Phe Ala Leu Ile Ile Leu Asn Cys Met
1               5                   10                  15

Asp Tyr Ser His Cys Gln Gly Asn Arg Trp Arg Arg Ser Lys Arg Ala
            20                  25                  30

Ser Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys
        35                  40                  45

Asp Asn Gly Cys Ser Arg Cys Gln Gln Lys Leu Phe Phe Phe Leu Arg
    50                  55                  60

Arg Glu Gly Met Arg Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser
65                  70                  75                  80
```

```
Gly Tyr Tyr Gly His Arg Ala Pro Asp Met Asn Arg Cys Ala Arg Cys
                85                  90                  95

Arg Ile Glu Asn Cys Asp Ser Cys Phe Ser Lys Asp Phe Cys Thr Lys
            100                 105                 110

Cys Lys Val Gly Phe Tyr Leu His Arg Gly Arg Cys Phe Asp Glu Cys
        115                 120                 125

Pro Asp Gly Phe Ala Pro Leu Glu Glu Thr Met Glu Cys Val Glu Gly
    130                 135                 140

Cys Glu Val Gly His Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn Asn
145                 150                 155                 160

Arg Thr Cys Gly Phe Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln Ile
                165                 170                 175

Val Lys Lys Pro Val Lys Asp Thr Ile Pro Cys Pro Thr Ile Ala Glu
            180                 185                 190

Ser Arg Arg Cys Lys Met Thr Met Arg His Cys Pro Gly Gly Lys Arg
        195                 200                 205

Thr Pro Lys Ala Lys Glu Lys Arg Asn Lys Lys Lys Lys Arg Lys Leu
    210                 215                 220

Ile Glu Arg Ala Gln Glu Gln His Ser Val Phe Leu Ala Thr Asp Arg
225                 230                 235                 240

Ala Asn Gln
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<210> 3
<211> 272
<212> PRT
<213> Homo sapiens

<400> 3

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Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1               5                   10                  15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
            20                  25                  30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
        35                  40                  45
```

```
Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
    50                  55                  60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65                  70                  75                  80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
                85                  90                  95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
            100                 105                 110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn
        115                 120                 125

Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser
    130                 135                 140

Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr
145                 150                 155                 160

Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val
                165                 170                 175

Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro
            180                 185                 190

Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys
        195                 200                 205

Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn
    210                 215                 220

Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser
225                 230                 235                 240

Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys
                245                 250                 255

Arg Lys Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His
            260                 265                 270
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<210> 4
<211> 234
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<213> Homo sapiens

<400> 4

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Met Arg Ala Pro Leu Cys Leu Leu Leu Leu Val Ala His Ala Val Asp
```

```
1               5                   10                  15

Met Leu Ala Leu Asn Arg Arg Lys Lys Gln Val Gly Thr Gly Leu Gly
            20                  25                  30

Gly Asn Cys Thr Gly Cys Ile Ile Cys Ser Glu Glu Asn Gly Cys Ser
        35                  40                  45

Thr Cys Gln Gln Arg Leu Phe Leu Phe Ile Arg Arg Glu Gly Ile Arg
    50                  55                  60

Gln Tyr Gly Lys Cys Leu His Asp Cys Pro Pro Gly Tyr Phe Gly Ile
65                  70                  75                  80

Arg Gly Gln Glu Val Asn Arg Cys Lys Lys Cys Gly Ala Thr Cys Glu
                85                  90                  95

Ser Cys Phe Ser Gln Asp Phe Cys Ile Arg Cys Lys Arg Gln Phe Tyr
            100                 105                 110

Leu Tyr Lys Gly Lys Cys Leu Pro Thr Cys Pro Pro Gly Thr Leu Ala
        115                 120                 125

His Gln Asn Thr Arg Glu Cys Gln Gly Glu Cys Glu Leu Gly Pro Trp
    130                 135                 140

Gly Gly Trp Ser Pro Cys Thr His Asn Gly Lys Thr Cys Gly Ser Ala
145                 150                 155                 160

Trp Gly Leu Glu Ser Arg Val Arg Glu Ala Gly Arg Ala Gly His Glu
                165                 170                 175

Glu Ala Ala Thr Cys Gln Val Leu Ser Glu Ser Arg Lys Cys Pro Ile
            180                 185                 190

Gln Arg Pro Cys Pro Gly Glu Arg Ser Pro Gly Gln Lys Lys Gly Arg
        195                 200                 205

Lys Asp Arg Arg Pro Arg Lys Asp Arg Lys Leu Asp Arg Arg Leu Asp
    210                 215                 220

Val Arg Pro Arg Gln Pro Gly Leu Gln Pro
225                 230
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<210> 5
<211> 243
<212> PRT
<213> Homo sapiens

<400> 5

Ser Arg Gly Ile Lys Gly Lys Arg Gln Arg Arg Ile Ser Ala Glu Gly
1 5 10 15

Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser Glu Val Asn Gly
20 25 30

Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu Glu Arg Asn Asp
35 40 45

Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro Pro Gly Tyr Phe
50 55 60

Asp Ala Arg Asn Pro Asp Met Asn Lys Cys Ile Lys Cys Lys Ile Glu
65 70 75 80

His Cys Glu Ala Cys Phe Ser His Asn Phe Cys Thr Lys Cys Lys Glu
85 90 95

Gly Leu Tyr Leu His Lys Gly Arg Cys Tyr Pro Ala Cys Pro Glu Gly
100 105 110

Ser Ser Ala Ala Asn Gly Thr Met Glu Cys Ser Ser Pro Ala Gln Cys
115 120 125

Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser Lys Lys Gln Gln
130 135 140

Leu Cys Gly Phe Arg Arg Gly Ser Glu Glu Arg Thr Arg Arg Val Leu
145 150 155 160

His Ala Pro Val Gly Asp His Ala Ala Cys Ser Asp Thr Lys Glu Thr
165 170 175

Arg Arg Cys Thr Val Arg Arg Val Pro Cys Pro Glu Gly Gln Lys Arg
180 185 190

Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn Ala Asn Arg Asn Leu Ala
195 200 205

Arg Lys Glu Ser Lys Glu Ala Gly Ala Gly Ser Arg Arg Arg Lys Gly
210 215 220

Gln Gln Gln Gln Gln Gln Gln Gly Thr Val Gly Pro Leu Thr Ser Ala
225 230 235 240

Gly Pro Ala

<210> 6
<211> 52
<212> PRT
<213> Homo sapiens

<400> 6

Ala Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu Cys Ser Glu
1 5 10 15

Val Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile Leu Leu Glu
20 25 30

Arg Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser Cys Pro Pro
35 40 45

Gly Tyr Phe Asp
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<210> 7
<211> 45
<212> PRT
<213> Homo sapiens

<400> 7

Met Asn Lys Cys Ile Lys Cys Lys Ile Glu His Cys Glu Ala Cys Phe
1 5 10 15

Ser His Asn Phe Cys Thr Lys Cys Lys Glu Gly Leu Tyr Leu His Lys
20 25 30

Gly Arg Cys Tyr Pro Ala Cys Pro Glu Gly Ser Ser Ala
35 40 45

<210> 8
<211> 61
<212> PRT
<213> Homo sapiens

<400> 8

Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro Cys Ser Lys Lys
1 5 10 15

Gln Gln Leu Cys Gly Phe Arg Arg Gly Ser Glu Glu Arg Thr Arg Arg
20 25 30

Val Leu His Ala Pro Val Gly Asp His Ala Ala Cys Ser Asp Thr Lys
35 40 45

Glu Thr Arg Arg Cys Thr Val Arg Arg Val Pro Cys Pro

```
    50                  55                  60

<210>  9
<211>  233
<212>  PRT
<213>  Homo sapiens

<400>  9

Arg Ile Ser Ala Glu Gly Ser Gln Ala Cys Ala Lys Gly Cys Glu Leu
1               5                   10                  15

Cys Ser Glu Val Asn Gly Cys Leu Lys Cys Ser Pro Lys Leu Phe Ile
            20                  25                  30

Leu Leu Glu Arg Asn Asp Ile Arg Gln Val Gly Val Cys Leu Pro Ser
        35                  40                  45

Cys Pro Pro Gly Tyr Phe Asp Ala Arg Asn Pro Asp Met Asn Lys Cys
    50                  55                  60

Ile Lys Cys Lys Ile Glu His Cys Glu Ala Cys Phe Ser His Asn Phe
65                  70                  75                  80

Cys Thr Lys Cys Lys Glu Gly Leu Tyr Leu His Lys Gly Arg Cys Tyr
                85                  90                  95

Pro Ala Cys Pro Glu Gly Ser Ser Ala Ala Asn Gly Thr Met Glu Cys
            100                 105                 110

Ser Ser Pro Ala Gln Cys Glu Met Ser Glu Trp Ser Pro Trp Gly Pro
        115                 120                 125

Cys Ser Lys Lys Gln Gln Leu Cys Gly Phe Arg Arg Gly Ser Glu Glu
    130                 135                 140

Arg Thr Arg Arg Val Leu His Ala Pro Val Gly Asp His Ala Ala Cys
145                 150                 155                 160

Ser Asp Thr Lys Glu Thr Arg Arg Cys Thr Val Arg Arg Val Pro Cys
                165                 170                 175

Pro Glu Gly Gln Lys Arg Arg Lys Gly Gly Gln Gly Arg Arg Glu Asn
            180                 185                 190

Ala Asn Arg Asn Leu Ala Arg Lys Glu Ser Lys Glu Ala Gly Ala Gly
        195                 200                 205

Ser Arg Arg Arg Lys Gly Gln Gln Gln Gln Gln Gln Gly Thr Val
    210                 215                 220
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Gly Pro Leu Thr Ser Ala Gly Pro Ala
225 230

<210> 10
<211> 121
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 10

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ser His Gly Lys Thr Leu Glu Trp Ile
35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Glu Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

Leu Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 11
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 11

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Asn Ile Thr Cys Lys Ala Ser Gln Asp Val Ile Phe Ala
20 25 30

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60

Ser Val Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 12
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 12

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Thr Gly Tyr Thr Met His
1               5
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<210> 13
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 13

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Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Asn Phe Lys
1               5                   10                  15

Gly
```

<210> 14
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 14

Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala Tyr
1 5 10

<210> 15
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 15

Lys Ala Ser Gln Asp Val Ile Phe Ala Val Ala
1 5 10

<210> 16
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 16

Trp Ala Ser Thr Arg His Thr
1 5

<210> 17
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 17

Gln Gln His Tyr Ser Thr Pro Trp
1 5

<210> 18
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 18

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 19
<211> 363
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 19
gaggtccagc tgcaacagtc tggacctgag ctggtgaagc ctggggcttc agtgaagata 60

tcctgcaaga cttctggata cacattcact ggatacacca tgcactgggt gaggcagagc 120

catggaaaga cccttgagtg gattggaggt attaatccta acaatggtgg tactacttac 180

aaccagaact tcaagggcaa ggccacattg actgtagaga agtcctccac cacagcctac 240

ttggagctcc gcagcctgac atctgaggat tctgcactct attactgtgc aagaaaggag 300

ttctctgatg gttactactt ttttgcttac tggggccaag ggactctggt cactgtctct 360

gca 363

<210> 20
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 20
gacattgtga tgacccagtc tcacaaattc atgtccacat cagtgggaga cagggtcaac 60

atcacctgca aggccagtca ggatgtgatt tttgctgtag cctggtatca acagaaacca 120

ggacaatctc ctaaactact gatttactgg gcatccaccc ggcacactgg agtccctgat 180

cgcttcacag gcagtgtatc tgggacagat tatactctca ccatcagcag tgtgcaggct 240

gaagacctgg cactttatta ctgtcagcaa cattatagca ctccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa a 321

<210> 21
<211> 464
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 21

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

Val Leu Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe
35 40 45

```
Thr Gly Tyr Thr Met His Trp Val Arg Gln Ser His Gly Lys Thr Leu
    50                  55                  60

Glu Trp Ile Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn
65                  70                  75                  80

Gln Asn Phe Lys Gly Lys Ala Thr Leu Thr Val Glu Lys Ser Ser Thr
                85                  90                  95

Thr Ala Tyr Leu Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Leu
            100                 105                 110

Tyr Tyr Cys Ala Arg Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr
    130                 135                 140

Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn
145                 150                 155                 160

Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val
        195                 200                 205

Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val
    210                 215                 220

Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg
225                 230                 235                 240

Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser
                245                 250                 255

Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu
            260                 265                 270

Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro
        275                 280                 285

Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala
    290                 295                 300
```

```
Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val
305                 310                 315                 320

Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe
                325                 330                 335

Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr
            340                 345                 350

Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile
        355                 360                 365

Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys
    370                 375                 380

Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp
385                 390                 395                 400

Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp
                405                 410                 415

Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser
            420                 425                 430

Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly
        435                 440                 445

Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
    450                 455                 460
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<210> 22
<211> 238
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 22

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Met Gly Phe Lys Met Glu Ser Gln Ile Gln Ala Phe Val Phe Val Phe
1               5                   10                  15

Leu Trp Leu Ser Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His
            20                  25                  30

Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Asn Ile Thr Cys Lys
        35                  40                  45

Ala Ser Gln Asp Val Ile Phe Ala Val Ala Trp Tyr Gln Gln Lys Pro
    50                  55                  60
```

```
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr
65                  70                  75                  80

Gly Val Pro Asp Arg Phe Thr Gly Ser Val Ser Gly Thr Asp Tyr Thr
                85                  90                  95

Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr Tyr Cys
            100                 105                 110

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
    130                 135                 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145                 150                 155                 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
                165                 170                 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
            180                 185                 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
        195                 200                 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
    210                 215                 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225                 230                 235
```

<210> 23
<211> 1398
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 23

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atgggatgga gctggatctt tctctttctc ctgtcaggaa ctgcaggtgt cctctctgag       60

gtccagctgc aacagtctgg acctgagctg gtgaagcctg gggcttcagt gaagatatcc      120

tgcaagactt ctggatacac attcactgga tacaccatgc actgggtgag gcagagccat      180

ggaaagaccc ttgagtggat tggaggtatt aatcctaaca atggtggtac tacttacaac      240

cagaacttca agggcaaggc cacattgact gtagagaagt cctccaccac agcctacttg      300
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gagctccgca gcctgacatc tgaggattct gcactctatt actgtgcaag aaaggagttc 360

tctgatggtt actacttttt tgcttactgg ggccaaggga ctctggtcac tgtctcttca 420

gccaaaacga cacccccatc tgtctatcca ctggcccctg gatctgctgc ccaaactaac 480

tccatggtga ccctgggatg cctggtcaag ggctatttcc ctgagccagt gacagtgacc 540

tggaactctg gatccctgtc cagcggtgtg cacaccttcc cagctgtcct gcagtctgac 600

ctctacactc tgagcagctc agtgactgtc ccctccagca cctggcccag cgagaccgtc 660

acctgcaacg ttgcccaccc ggccagcagc accaaggtgg acaagaaaat tgtgcccagg 720

gattgtggtt gtaagccttg catatgtaca gtcccagaag tatcatctgt cttcatcttc 780

cccccaaagc ccaaggatgt gctcaccatt actctgactc ctaaggtcac gtgtgttgtg 840

gtagacatca gcaaggatga tcccgaggtc agttcagct ggtttgtaga tgatgtggag 900

gtgcacacag ctcagacgca accccgggag gagcagttca acagcacttt ccgctcagtc 960

agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggtc 1020

aacagtgcag ctttccctgc ccccatcgag aaaaccatct ccaaaaccaa aggcagaccg 1080

aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaagtc 1140

agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtgg 1200

aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct 1260

tacttcgtct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc 1320

acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctcccac 1380

tctcctggta aatgataa 1398

<210> 24
<211> 720
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 24
atgggcttca agatggagtc acagattcag gcatttgtat tcgtgtttct ctggttgtct 60

ggtgttgacg gagacattgt gatgacccag tctcacaaat tcatgtccac atcagtggga 120

gacagggtca acatcacctg caaggccagt caggatgtga tttttgctgt agcctggtat 180

caacagaaac caggacaatc tcctaaacta ctgatttact gggcatccac ccggcacact 240

ggagtccctg atcgcttcac aggcagtgta tctgggacag attatactct caccatcagc 300

agtgtgcagg ctgaagacct ggcactttat tactgtcagc aacattatag cactccgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttagtga 720

<210> 25
<211> 445
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 25

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Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1               5                  10                  15

Ser Val Lys Ile Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Thr Met His Trp Val Arg Gln Ser His Gly Lys Thr Leu Glu Trp Ile
        35                  40                  45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Asn Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Glu Lys Ser Ser Thr Thr Ala Tyr
65                  70                  75                  80

Leu Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Arg Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser
        115                 120                 125

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
    130                 135                 140

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
```

```
Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro
            180                 185                 190

Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro
        195                 200                 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly
    210                 215                 220

Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
                245                 250                 255

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
            260                 265                 270

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
    290                 295                 300

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
305                 310                 315                 320

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro
            340                 345                 350

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
        355                 360                 365

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
    370                 375                 380

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
385                 390                 395                 400

Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
                405                 410                 415

Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
            420                 425                 430
```

```
His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445


<210>  26
<211>  214
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Misc.

<400>  26

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1               5                   10                  15


Asp Arg Val Asn Ile Thr Cys Lys Ala Ser Gln Asp Val Ile Phe Ala
            20                  25                  30


Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
    50                  55                  60


Ser Val Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80


Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
            100                 105                 110


Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
        115                 120                 125


Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
    130                 135                 140


Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145                 150                 155                 160


Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175


Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190


Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205
```

Phe Asn Arg Asn Glu Cys
210

<210> 27
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 27

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Phe Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Phe Cys Ala
85 90 95

Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu Asp Ala Met
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120 125

<210> 28
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 28

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ser Ala
20 25 30

```
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Asn
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 29
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 29

```
Ser Ser Tyr Ala Met Ser
1               5
```

<210> 30
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 30

```
Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys Gly
1               5                   10                  15
```

<210> 31
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 31

```
Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu Asp Ala Met
1               5                   10                  15
```

Asp Tyr

<210> 32
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 32

Lys Ala Ser Gln Asp Val Ser Ser Ala Val Ala
1 5 10

<210> 33
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 33

Trp Ala Ser Thr Arg His Thr
1 5

<210> 34
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 34

Gln Gln His Tyr Ser Thr Pro
1 5

<210> 35
<211> 375
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 35
gaagtgaagc tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaattt 60

tcctgtgcag cctctggatt cagtttcagt agttatgcca tgtcttgggt tcgccagact 120

ccagagaaga ggctggagtg ggtcgcatcc attagtagtg gtggtagtac ctactatcca 180

gacagtgtga agggccgatt caccatctcc agagataatg tcaggaacat cctgtacctg 240

caaatgagca gtctgaggtc tgaggacacg gccatgtatt tctgtgcacg aggcggggat 300

ccgggggtct acaatggtga ctacgaagat gctatggact actggggtca aggaacctca 360

gtcaccgtct cctca 375

<210> 36
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 36
gacattgtga tgacccagtc tcacaaattc atgtccacat cagtcggaga cagggtcagc 60

atcacctgca aggccagtca ggatgtgagt tctgctgtag cctggtatca acaaaaacca 120

gggcaatctc ctaaactact gatttactgg gcatccaccc ggcacactgg agtccctgat 180

cgcttcacaa acagtggatc tgggacagat tatactctca ccatcagtag tgtgcaggct 240

gaagacctgg cactttatta ctgtcagcaa cattatagca ctccgtggac gttcggtgga 300

ggcaccaagc tggaaatcaa a 321

<210> 37
<211> 468
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 37

Met Asn Phe Gly Leu Arg Leu Val Phe Leu Val Leu Val Leu Lys Gly
1 5 10 15

Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Lys Phe Ser Cys Ala Ala Ser Gly Phe Ser Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
50 55 60

Glu Trp Val Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile
85 90 95

Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr
100 105 110

```
Phe Cys Ala Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu
        115                 120                 125

Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
    130                 135                 140

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
145                 150                 155                 160

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
        195                 200                 205

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
    210                 215                 220

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
225                 230                 235                 240

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
                245                 250                 255

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
            260                 265                 270

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
        275                 280                 285

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
    290                 295                 300

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
305                 310                 315                 320

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
                325                 330                 335

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
            340                 345                 350

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
        355                 360                 365
```

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
370 375 380

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
385 390 395 400

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
405 410 415

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
420 425 430

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
435 440 445

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
450 455 460

Ser Pro Gly Lys
465

<210> 38
<211> 238
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 38

Met Gly Ile Lys Met Glu Ser Gln Ile Gln Ala Phe Val Phe Val Phe
1 5 10 15

Leu Trp Leu Ser Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser His
20 25 30

Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys
35 40 45

Ala Ser Gln Asp Val Ser Ser Ala Val Ala Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Asn Ser Gly Ser Gly Thr Asp Tyr Thr
85 90 95

```
Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr Tyr Cys
            100                 105                 110

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
        115                 120                 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
    130                 135                 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145                 150                 155                 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
                165                 170                 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
            180                 185                 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
        195                 200                 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
    210                 215                 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
225                 230                 235
```

<210> 39
<211> 1407
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 39

```
atgaacttcg ggctgagatt ggttttcctt gtccttgttt taaaaggtgt ccagtgtgaa       60

gtgaagctgg tggagtctgg gggaggctta gtgaagcctg gagggtccct gaaattttcc      120

tgtgcagcct ctggattcag tttcagtagt tatgccatgt cttgggttcg ccagactcca      180

gagaagaggc tggagtgggt cgcatccatt agtagtggtg gtagtaccta ctatccagac      240

agtgtgaagg gccgattcac catctccaga gataatgtca ggaacatcct gtacctgcaa      300

atgagcagtc tgaggtctga ggacacggcc atgtatttct gtgcacgagg cggggatccg      360

ggggtctaca atggtgacta cgaagatgct atggactact ggggtcaagg aacctcagtc      420

accgtctcct cagccaaaac gacaccccca tctgtctatc cactggcccc tggatctgct      480

gcccaaacta actccatggt gaccctggga tgcctggtca agggctattt ccctgagcca      540

gtgacagtga cctggaactc tggatccctg tccagcggtg tgcacacctt cccagctgtc      600
```

ctgcagtctg acctctacac tctgagcagc tcagtgactg tcccctccag cacctggccc 660

agcgagaccg tcacctgcaa cgttgcccac ccggccagca gcaccaaggt ggacaagaaa 720

attgtgccca gggattgtgg ttgtaagcct tgcatatgta cagtcccaga agtatcatct 780

gtcttcatct tccccccaaa gcccaaggat gtgctcacca ttactctgac tcctaaggtc 840

acgtgtgttg tggtagacat cagcaaggat gatcccgagg tccagttcag ctggtttgta 900

gatgatgtgg aggtgcacac agctcagacg caaccccggg aggagcagtt caacagcact 960

ttccgctcag tcagtgaact tcccatcatg caccaggact ggctcaatgg caaggagttc 1020

aaatgcaggg tcaacagtgc agctttccct gcccccatcg agaaaaccat ctccaaaacc 1080

aaaggcagac cgaaggctcc acaggtgtac accattccac ctcccaagga gcagatggcc 1140

aaggataaag tcagtctgac ctgcatgata acagacttct tccctgaaga cattactgtg 1200

gagtggcagt ggaatgggca gccagcggag aactacaaga acactcagcc catcatggac 1260

acagatggct cttacttcgt ctacagcaag ctcaatgtgc agaagagcaa ctgggaggca 1320

ggaaatactt tcacctgctc tgtgttacat gagggcctgc acaaccacca tactgagaag 1380

agcctctccc actctcctgg taaatga 1407

<210> 40
<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 40
atgggcatca agatggagtc acagattcag gcatttgtat tcgtgtttct ctggttgtct 60

ggtgttgacg gagacattgt gatgacccag tctcacaaat tcatgtccac atcagtcgga 120

gacagggtca gcatcacctg caaggccagt caggatgtga gttctgctgt agcctggtat 180

caacaaaaac cagggcaatc tcctaaacta ctgatttact gggcatccac ccggcacact 240

ggagtccctg atcgcttcac aaacagtgga tctgggacag attatactct caccatcagt 300

agtgtgcagg ctgaagacct ggcactttat tactgtcagc aacattatag cactccgtgg 360

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660

actcacaaga catcaacttc acccattgtc aagagcttca acaggaatga gtgttag 717

<210> 41
<211> 449
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 41

Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Phe Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Arg Asn Ile Leu Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Phe Cys Ala
85 90 95

Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu Asp Ala Met
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr
115 120 125

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
130 135 140

Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
180 185 190

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
195 200 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
210 215 220

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
245 250 255

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
260 265 270

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
275 280 285

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
290 295 300

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
340 345 350

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
355 360 365

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
370 375 380

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
385 390 395 400

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
405 410 415

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
420 425 430

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
435 440 445

Lys

<210> 42
<211> 214

<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 42

```
Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
1               5                  10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ser Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Asn
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala
            100                 105                 110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
        115                 120                 125

Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile
    130                 135                 140

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145                 150                 155                 160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165                 170                 175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180                 185                 190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195                 200                 205

Phe Asn Arg Asn Glu Cys
    210
```

<210> 43
<211> 222
<212> PRT
<213> Homo sapiens

<400> 43

Gln Gly Asn Arg Trp Arg Arg Ser Lys Arg Ala Ser Tyr Val Ser Asn
1 5 10 15

Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys Asp Asn Gly Cys Ser
20 25 30

Arg Cys Gln Gln Lys Leu Phe Phe Phe Leu Arg Arg Glu Gly Met Arg
35 40 45

Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser Gly Tyr Tyr Gly His
50 55 60

Arg Ala Pro Asp Met Asn Arg Cys Ala Arg Cys Arg Ile Glu Asn Cys
65 70 75 80

Asp Ser Cys Phe Ser Lys Asp Phe Cys Thr Lys Cys Lys Val Gly Phe
85 90 95

Tyr Leu His Arg Gly Arg Cys Phe Asp Glu Cys Pro Asp Gly Phe Ala
100 105 110

Pro Leu Glu Glu Thr Met Glu Cys Val Glu Gly Cys Glu Val Gly His
115 120 125

Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn Asn Arg Thr Cys Gly Phe
130 135 140

Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln Ile Val Lys Lys Pro Val
145 150 155 160

Lys Asp Thr Ile Pro Cys Pro Thr Ile Ala Glu Ser Arg Arg Cys Lys
165 170 175

Met Thr Met Arg His Cys Pro Gly Gly Lys Arg Thr Pro Lys Ala Lys
180 185 190

Glu Lys Arg Asn Lys Lys Lys Lys Arg Lys Leu Ile Glu Arg Ala Gln
195 200 205

Glu Gln His Ser Val Phe Leu Ala Thr Asp Arg Ala Asn Gln
210 215 220

<210> 44

<211> 184
<212> PRT
<213> Homo sapiens

<400> 44

Gln Gly Asn Arg Trp Arg Arg Ser Lys Arg Ala Ser Tyr Val Ser Asn
1 5 10 15

Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys Asp Asn Gly Cys Ser
20 25 30

Arg Cys Gln Gln Lys Leu Phe Phe Phe Leu Arg Arg Glu Gly Met Arg
35 40 45

Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser Gly Tyr Tyr Gly His
50 55 60

Arg Ala Pro Asp Met Asn Arg Cys Ala Arg Cys Arg Ile Glu Asn Cys
65 70 75 80

Asp Ser Cys Phe Ser Lys Asp Phe Cys Thr Lys Cys Lys Val Gly Phe
85 90 95

Tyr Leu His Arg Gly Arg Cys Phe Asp Glu Cys Pro Asp Gly Phe Ala
100 105 110

Pro Leu Glu Glu Thr Met Glu Cys Val Glu Gly Cys Glu Val Gly His
115 120 125

Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn Asn Arg Thr Cys Gly Phe
130 135 140

Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln Ile Val Lys Lys Pro Val
145 150 155 160

Lys Asp Thr Ile Pro Cys Pro Thr Ile Ala Glu Ser Arg Arg Cys Lys
165 170 175

Met Thr Met Arg His Cys Pro Gly
180

<210> 45
<211> 51
<212> PRT
<213> Homo sapiens

<400> 45

Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys Asp
1 5 10 15

```
Asn Gly Cys Ser Arg Cys Gln Gln Lys Leu Phe Phe Phe Leu Arg Arg
            20                  25                  30

Glu Gly Met Arg Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser Gly
        35                  40                  45

Tyr Tyr Gly
    50
```

<210> 46
<211> 45
<212> PRT
<213> Homo sapiens

<400> 46

```
Met Asn Arg Cys Ala Arg Cys Arg Ile Glu Asn Cys Asp Ser Cys Phe
1               5                   10                  15

Ser Lys Asp Phe Cys Thr Lys Cys Lys Val Gly Phe Tyr Leu His Arg
            20                  25                  30

Gly Arg Cys Phe Asp Glu Cys Pro Asp Gly Phe Ala Pro
        35                  40                  45
```

<210> 47
<211> 61
<212> PRT
<213> Homo sapiens

<400> 47

```
Gly Cys Glu Val Gly His Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn
1               5                   10                  15

Asn Arg Thr Cys Gly Phe Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln
            20                  25                  30

Ile Val Lys Lys Pro Val Lys Asp Thr Ile Pro Cys Pro Thr Ile Ala
        35                  40                  45

Glu Ser Arg Arg Cys Lys Met Thr Met Arg His Cys Pro
    50                  55                  60
```

<210> 48
<211> 251
<212> PRT
<213> Homo sapiens

<400> 48

```
Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His Pro Asn Val
1               5                   10                  15
```

Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp Tyr Asn Gly
20 25 30

Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu Arg Ile Gly
35 40 45

Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser Gly Tyr Tyr
50 55 60

Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp
65 70 75 80

Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly
85 90 95

Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu
100 105 110

Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val His Cys Glu
115 120 125

Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys Gly Lys Thr
130 135 140

Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu Ile Ile Gln
145 150 155 160

His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn Glu Thr Arg
165 170 175

Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu Arg Gly Lys
180 185 190

Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly Glu Ser Lys
195 200 205

Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys Glu Ile Pro
210 215 220

Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys Val Gln Asp
225 230 235 240

Lys Gln Lys Ser Val Ser Val Ser Thr Val His
245 250

<210> 49
<211> 52

<212> PRT
<213> Homo sapiens

<400> 49

Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp
1 5 10 15

Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu
20 25 30

Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser
35 40 45

Gly Tyr Tyr Gly
50

<210> 50
<211> 44
<212> PRT
<213> Homo sapiens

<400> 50

Ile Asn Lys Cys Thr Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn
1 5 10 15

Lys Asn Phe Cys Thr Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly
20 25 30

Lys Cys Leu Asp Asn Cys Pro Glu Gly Leu Glu Ala
35 40

<210> 51
<211> 61
<212> PRT
<213> Homo sapiens

<400> 51

His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys
1 5 10 15

Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu
20 25 30

Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn
35 40 45

Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln
50 55 60

<210> 52

<211> 1401
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 52
atggactgga cctggaggat actctttctc gtggcagcag ccacaggagc ccactcccag 60

gtccagctcg tgcagtctgg ggctgaggtg aagaagcctg gggcctctgt gaaggtttcc 120

tgcaagactt ctggatacac cttcactgga tacaccatgc actgggttag acaggccccc 180

ggacaaaggc tggagtggat gggaggtatt aatcctaaca atggtggtac tacttacaac 240

cagaacttca agggcagagt caccattacc agggacacat ccgcaagcac agcctacatg 300

gagctgtcca gcctgagatc tgaagacaca gctgtgtatt actgtgcaag aaaggagttc 360

tctgatggat actacttttt tgcttactgg ggccaaggga ccctggtcac cgtcagctca 420

gccagcacaa agggccctag cgtcttccct ctggctccct gcagcaggag caccagcgag 480

agcacagccg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca 600

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc 660

tacacctgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 720

aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc 780

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc 840

gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc 900

gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt 960

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 1020

aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg 1080

cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 1140

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 1200

gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 1260

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1320

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1380

tccctgtctc cgggtaaatg a 1401

<210> 53
<211> 466
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 53

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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1               5                  10                  15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            20                  25                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe
        35                  40                  45

Thr Gly Tyr Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
    50                  55                  60

Glu Trp Met Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn
65                  70                  75                  80

Gln Asn Phe Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser
                85                  90                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            100                 105                 110

Tyr Tyr Cys Ala Arg Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala
        115                 120                 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
    130                 135                 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
145                 150                 155                 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205

Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn
    210                 215                 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg
225                 230                 235                 240

Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
```

245 250 255

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
260 265 270

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
275 280 285

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
290 295 300

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
305 310 315 320

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
325 330 335

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
340 345 350

Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
355 360 365

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
370 375 380

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
385 390 395 400

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
405 410 415

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
420 425 430

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
435 440 445

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
450 455 460

Gly Lys
465

<210> 54
<211> 363
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 54
caggtccagc tcgtgcagtc tggggctgag gtgaagaagc ctggggcctc tgtgaaggtt 60

tcctgcaaga cttctggata caccttcact ggatacacca tgcactgggt tagacaggcc 120

cccggacaaa ggctggagtg gatgggaggt attaatccta acaatggtgg tactacttac 180

aaccagaact tcaagggcag agtcaccatt accagggaca catccgcaag cacagcctac 240

atggagctgt ccagcctgag atctgaagac acagctgtgt attactgtgc aagaaaggag 300

ttctctgatg gatactactt ttttgcttac tggggccaag ggaccctggt caccgtcagc 360

tca 363

<210> 55
<211> 121
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 55

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 56
<211> 711
<212> DNA

<213> Artificial sequence

<220>
<223> Misc.

<400> 56
atggacatga gggtccccgc acagctcctg gggctcctgc tcctctggct ccggggtgcc 60

agatgtgaca tccagatgac ccagtctcca tcctccctgt ctgcatctgt cggagacaga 120

gtcaccatca cttgcaaggc ctcccaggat gtgatttttg ctgttgcctg gtatcagcag 180

aaaccaggga aagcccctaa gctcctgatc tattgggcat ccacccggca cactggggtc 240

ccatcaaggt tcagtggcag tggatctggg acagattaca ctctcaccat cagcagtctg 300

caacctgaag attttgcaac ttactactgt cagcaacatt atagcactcc ttggactttc 360

ggcggaggga ccaaggtgga gatcaaacgg actgtggctg caccatctgt cttcatcttc 420

cctccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtccagtgg aaggtggata acgccctcca atccggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcaacacc 600

ctgacactga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcccccgt cacaaagagc ttcaacaggg gagagtgcta a 711

<210> 57
<211> 236
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 57

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45

Gln Asp Val Ile Phe Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 58
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 58
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtcggaga cagagtcacc 60

atcacttgca aggcctccca ggatgtgatt tttgctgttg cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattgg gcatccaccc ggcacactgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat tacactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcagcaa cattatagca ctccttggac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 59
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 59

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ile Phe Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 60
<211> 1413
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 60
atggaactgg gactcagatg ggttttcctc gttgctattc tggaaggagt ccagtgtgag 60

gtgcagctgg tggagtctgg gggaggcctg gtcaagcctg gaggatctct gcggctctcc 120

tgtgcagcct ctggattcac cttctcctct tatgccatgt cttgggtccg gcaggctcca 180

gggaaggggc tggaatgggt ctcatccatt tctagtggag gtagcacata ttatcctgac 240

agcgtgaagg gccggttcac catctccaga gacaacgcca agaacagcct gtatctgcaa 300

atgaacagcc tgagagccga ggacacagct gtgtattact gtgctagagg tggagatcct 360

ggggtctaca atggagatta cgaagatgct atggactact gggggcaagg aacaacagtc 420

acagtcagct cagccagcac aaagggccct agcgtcttcc ctctggctcc ctgcagcagg 480

agcaccagcg agagcacagc cgccctgggc tgcctggtca aggactactt ccccgaaccg 540

gtgacggtgt cgtggaactc aggcgctctg accagcggcg tgcacacctt cccagctgtc 600

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcaacttc 660

ggcacccaga cctacacctg caacgtagat cacaagccca gcaacaccaa ggtggacaag 720

acagttgagc gcaaatgttg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 780

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccccc 840

gaggtcacgt gcgtggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 900

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 960

agcacgttcc gtgtggtcag cgtcctcacc gttgtgcacc aggactggct gaacggcaag 1020

gagtacaagt gcaaggtctc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc 1080

aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 1140

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1200

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1260

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1320

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1380

cagaagagcc tctccctgtc tccgggtaaa tga 1413

<210> 61
<211> 470
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 61

Met Glu Leu Gly Leu Arg Trp Val Phe Leu Val Ala Ile Leu Glu Gly
1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Val Ser Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp
65 70 75 80

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser
85 90 95

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
100 105 110

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Tyr Cys Ala Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu
        115                 120                 125

Asp Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
    130                 135                 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
145                 150                 155                 160

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
                165                 170                 175

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
            180                 185                 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
        195                 200                 205

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
    210                 215                 220

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
225                 230                 235                 240

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
                245                 250                 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
    290                 295                 300

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
305                 310                 315                 320

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
                325                 330                 335

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
            340                 345                 350

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
        355                 360                 365
```

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
370 375 380

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385 390 395 400

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
405 410 415

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
450 455 460

Ser Leu Ser Pro Gly Lys
465 470

<210> 62
<211> 375
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 62
gaggtgcagc tggtggagtc tgggggaggc ctggtcaagc ctggaggatc tctgcggctc 60

tcctgtgcag cctctggatt caccttctcc tcttatgcca tgtcttgggt ccggcaggct 120

ccagggaagg ggctggaatg ggtctcatcc atttctagtg gaggtagcac atattatcct 180

gacagcgtga agggccggtt caccatctcc agagacaacg ccaagaacag cctgtatctg 240

caaatgaaca gcctgagagc cgaggacaca gctgtgtatt actgtgctag aggtggagat 300

cctggggtct acaatggaga ttacgaagat gctatggact actgggggca aggaacaaca 360

gtcacagtca gctca 375

<210> 63
<211> 125
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 63

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu Asp Ala Met
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 64
<211> 711
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 64
atgaaatacc tcctccctac agctgccgct ggactcctcc tcctcgctgc ccagcctgcc 60

atggccgaca tccagatgac ccagtcccct tcctccctgt ctgcttccgt cggagacaga 120

gtcaccatca cttgcaaggc ctcccaggat gtgtcctctg ctgtcgcttg gtatcagcag 180

aaaccaggaa aagctcctaa gctcctgatc tattgggcat ccaccaggca cacaggagtc 240

ccttccaggt tctccggctc tggatctggg acagatttca ctctcaccat cagctccgtg 300

caagctgaag attttgcaac ttactactgt cagcaacatt atagcactcc ttggacattc 360

ggacaaggga ccaaggtgga aatcaaaaga actgtggctg caccttctgt cttcatcttc 420

cctccatctg atgagcagct caaatctgga actgcctccg ttgtgtgcct gctgaataac 480

ttctatccta gagaggccaa agtccagtgg aaggtggata acgccctcca atccggtaac 540

tcccaggagt ctgtcacaga gcaggactcc aaggacagca cctactccct cagcaacacc 600

ctgacactgt ctaaagctga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggactga gctcccccgt cacaaaatcc ttcaacaggg gagagtgcta a 711

<210> 65
<211> 236
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 65

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
35 40 45

Gln Asp Val Ser Ser Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

Ile Ser Ser Val Gln Ala Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
100 105 110

His Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser

210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 66
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 66
gacatccaga tgacccagtc cccttcctcc ctgtctgctt ccgtcggaga cagagtcacc 60

atcacttgca aggcctccca ggatgtgtcc tctgctgtcg cttggtatca gcagaaacca 120

ggaaaagctc ctaagctcct gatctattgg gcatccacca ggcacacagg agtcccttcc 180

aggttctccg gctctggatc tgggacagat ttcactctca ccatcagctc cgtgcaagct 240

gaagattttg caacttacta ctgtcagcaa cattatagca ctccttggac attcggacaa 300

gggaccaagg tggaaatcaa a 321

<210> 67
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 67

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100 105

<210> 68
<211> 447
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 68

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
35 40 45

Gly Gly Ile Asn Pro Asn Asn Gly Gly Thr Thr Tyr Asn Gln Asn Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Lys Glu Phe Ser Asp Gly Tyr Tyr Phe Phe Ala Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

```
Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
    210                 215                 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
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<210> 69
<211> 214
<212> PRT

<213> Artificial sequence

<220>
<223> Misc.

<400> 69

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ile Phe Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 70

<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 70

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gly Gly Asp Pro Gly Val Tyr Asn Gly Asp Tyr Glu Asp Ala Met
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220
```

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 71
<211> 214
<212> PRT

<213> Artificial sequence

<220>
<223> Misc.

<400> 71

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ser Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 72

<211> 717
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 72
atgggcatca agatggagtc acagattcag gcatttgtat tcgtgtttct ctggttgtct 60

ggtgttgacg gagacatcca gatgacccag tcccttcct ccctgtctgc ttccgtcgga 120

gacagagtca ccatcacttg caaggcctcc caggatgtgt cctctgctgt cgcttggtat 180

cagcagaaac caggaaaagc tcctaagctc ctgatctatt gggcatccac caggcacaca 240

ggagtccctt ccaggttctc cggctctgga tctgggacag atttcactct caccatcagc 300

tccctgcaac ctgaagattt tgcaacttac tactgtcagc aacattatag cactccttgg 360

acattcggac aagggaccaa ggtggaaatc aaaagaactg tggctgcacc ttctgtcttc 420

atcttccctc catctgatga gcagctcaaa tctggaactg cctccgttgt gtgcctgctg 480

aataacttct atcctagaga ggccaaagtc cagtggaagg tggataacgc cctccaatcc 540

ggtaactccc aggagtctgt cacagagcag gactccaagg acagcaccta ctccctcagc 600

aacaccctga cactgtctaa agctgactac gagaaacaca aagtctacgc ctgcgaagtc 660

acccatcagg gactgagctc ccccgtcaca aaatccttca acaggggaga gtgctaa 717

<210> 73
<211> 238
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 73

Met Gly Ile Lys Met Glu Ser Gln Ile Gln Ala Phe Val Phe Val Phe
1 5 10 15

Leu Trp Leu Ser Gly Val Asp Gly Asp Ile Gln Met Thr Gln Ser Pro
20 25 30

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
35 40 45

Ala Ser Gln Asp Val Ser Ser Ala Val Ala Trp Tyr Gln Gln Lys Pro
50 55 60

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His Thr
65 70 75 80

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

85 90 95

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
100 105 110

Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Val
115 120 125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Asn Thr Leu Thr Leu Ser Lys Ala
195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 74
<211> 214
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 74

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ser Ala
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Asn Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 75
<211> 321
<212> DNA
<213> Artificial sequence

<220>
<223> Misc.

<400> 75
gacatccaga tgacccagtc cccttcctcc ctgtctgctt ccgtcggaga cagagtcacc 60

atcacttgca aggcctccca ggatgtgtcc tctgctgtcg cttggtatca gcagaaacca 120

ggaaaagctc ctaagctcct gatctattgg gcatccacca ggcacacagg agtcccttcc 180

aggttctccg gctctggatc tgggacagat ttcactctca ccatcagctc cctgcaacct 240

gaagattttg caacttacta ctgtcagcaa cattatagca ctccttggac attcggacaa 300

gggaccaagg tggaaatcaa a 321

<210> 76

<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Misc.

<400> 76

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Ser Ala
            20                  25                  30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```